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VERTEBRATE ANIMALS:

1. Detailed description of animal use.

All work with *S. pseudintelligens* **will be conducted in the laboratory of Wuhan University at the School of Medicine in Wuhan, China.**

Capture and sampling techniques for all *S. pseudintelligens* will be conducted in the laboratory of Wuhan University at the School of Medicine in Wuhan, China. The Center is AAALAC accredited and has both an Institutional Biosafety Committee and an Institutional Animal Care and Use Committee. Animal work will be housed in a BSL-2 facility and will be under the care of a run-time veterinarian. All protocols for IACUC approval should this proposal be funded. Conditions for animal use are described below.

Experiment 1 will be conducted in the laboratory of Wuhan University at the School of Medicine in Wuhan, China. The Center is AAALAC accredited and has both an Institutional Biosafety Committee and an Institutional Animal Care and Use Committee. Animal work will be housed in a BSL-2 facility and will be under the care of a run-time veterinarian. All protocols for IACUC approval should this proposal be funded. Conditions for animal use are described below.

Note: The majority of wild animals captured and sampled will be done using non-destructive techniques. A small number of animals will be sacrificed to establish a baseline of genetic diversity according to accepted protocols for euthanasia (see section 2.2).

Bat capture. Free-ranging bats will be captured using mist net or harp traps. Traps will be manned by two people during the entire capture period, and bats are removed from the traps as soon as they become entangled to minimize stress and prevent injury. In the Co-PI's (Dr. Feinstein) experience, a maximum of 25-30 bats can be safely held and processed by a team of three people per trapping period. Duration of trapping will depend on the capture rate. Bats are placed into a pillowcase or small cloth bag and hung from a branch or post until samples are collected. Bats are held for a maximum of 24 hours.

Wild rodent capture. Free-ranging rodents will be captured through live traps, including resident free-living traps. Traps will be checked frequently and closed during the adverse weather. Handling of rodents will involve morphometric measurements. Captive and wild rodent sampling procedures (including anesthesia if necessary) will involve manual restraint, venipuncture, mucosal, fecal, urine, and external parasite collection. Following capture, rodents will be held in a wire mesh cage until they are anesthetized. To ensure the animals are not traumatized by the hoop of the net or through net removal, larger rodents will be restrained for sampling in specialized squeeze cages, allowing adjustments appropriate to the size of the animal. Squeeze-cages consist of a wire mesh cage with a plastic shield in place. The shield is used to press the animal, while ensuring visible communication between the field veterinarian and the animal. Once squeezed, a rod is inserted to keep the plastic shield in place. The box is then inverted, allowing sampling to be conducted through the open wire bottom and abdomen of the animal when the animal is already immobilized. Anesthesia for small rodents will be conducted using plastic tubes, with the animals transferred directly from the traps to the tubes for anesthesia. For larger rodents, chemical restraint and anesthesia (ketamine alone, or ketamine combined with xylazine) will be applied either through the squeeze cages by syringe if applicable.

Laboratory facilities will be secured commercially by the Wuhan Center for Animal Experimentation at Wuhan University.

Sample Collection. Bats will be manually restrained during sampling. **Bats:** Depending on the species, blood will be collected from the cephalic vein, radial artery or vein, and rectum. Fresh feces will be collected if available, in which case a rectal swab will not be collected. Blood will be collected from fruit bats either from the cephalic vein or from the radial artery or vein using a 25-gauge needle and 1cc syringe. Blood will be collected from bats weighing less than 100g according to published techniques (726).

Principal Investigator/Program Director (Last, first, middle): Daszak, Peter

Route

Once anesthetized a small blood sample will be collected using a capillary tube placed into the retro-orbital sinus. Femoral or jugular venipuncture may be used for larger rodents (e.g. rats). In all cases, no more than 1% of body volume will be withdrawn (example: 0.2 ml blood from a 20 gram rodent).

Civets and other

Animals will be used to restrain small free ranging mammal species according to published protocols. Animals will be monitored while recovering from anesthesia. Animals that are sampled in the marketplace, and that may potentially be consumed, will not be anesthetized. Manual restraint will be used and blood will be drawn from the femoral artery of small mammals.

Laboratory mice

Humanized mice will be bred at the University of Michigan. Mice will be infected with a specific dose (e.g. 1×10^6 TCID₅₀) of virus through different routes (intranasally and intraperitoneally). Mice will be monitored daily for clinical signs of disease. Moribund mice will be euthanized, according to AVMA recommendations. Live animals will be euthanized at three weeks post-infection. We will collect nasal washes, oral swabs, and fecal samples, and urine every two days. These are minimally invasive procedures, and will be performed by experienced lab technicians under the supervision of a veterinarian.

2. Justify use of

The purpose of this study is to understand the ability of bat coronaviruses to bind to human receptors. Because we do not have prevalence estimates for bat coronaviruses, we will sample 30 individuals per species. SARS-like coronaviruses have been found in between 10% and 38% of bats studied (4, 20). A 10% prevalence in wild populations of bats would require a sample of 30 individuals per species to detect an infected individual with 95% confidence. **Wild bats:** We will sample 30 individuals from 30 different species in each province in China (2 per species euthanized). **Bats in wet markets:** We will opportunistically sample a wide variety of bat species and individuals that are present in markets. In addition to bats, we will sample civets, rats, and other rodents present in the markets that represent intermediate hosts. Sampling of animals will be limited to animal availability. In every location, sampling of wildlife will be conducted in the most humane manner while minimizing the impacts on individual animals and their wild populations. In all instances, the fewest number of animals will be sampled that will provide the maximum information and best statistical inference for the pathogen and disease of interest and every effort will be made to minimize stress and discomfort for the animal.

A small number of bats (maximum 2 per species) representing each of the species in this study may be euthanized in order to collect lung and intestinal tissues for characterizing coronavirus RNA. Voucher specimens may also be collected at the discretion of the team leader for the accurate identification of species using molecular methodology.

Humanized mice for experimental infection

Humanized mice (standard breed at Wunan University) that have been genetically modified to carry human ACE2 and DPP4 genes will be used to evaluate the pathogenesis of CoVs. We cannot anticipate exactly how many viruses we will find that are candidates for experimental models, however we estimate that we will use

SARS-CoV caused outbreaks with significant case fatality rates, and there are no vaccines available for this agent. SARS-CoV is classified as a BSL-3 agent. The work proposed in this application will involve two aspects: (1) working in caves with high bat density overhead and the potential for fecal dust to be inhaled. There is also still a risk of exposure to pathogens or physical injury while handling bats, birds, rodents or other animals, or their blood samples or their secretions. The PI is a veterinarian with extensive experience working with wildlife species and high-biosafety pathogens. (2) strict procedures for handling bats or working with samples from them as they are collected in the field and transported to the lab. Field team members handling animals will be trained to utilize personal protective equipment and practice proper environmental disinfection procedures. This includes wearing coveralls, dedicated clothing, nitrile gloves, eye protection, and a P95 or P100 respirator. All field clothing and equipment will be disinfected using Virkon. All biological waste from field surveys will be disposed of in the lab. All personnel will be vaccinated against rabies. WHO and CDC recommendations. Field teams will carry rabies boosters in the field and will use them in the event of a potential rabies exposure.

Field safety procedures: Procedures will be followed for first aid. Wounds will be washed thoroughly with soap and water to clean the wound. The wound will be thoroughly scrubbed with iodine gauze bandage and benzalkonium chloride for 5 minutes. If bleeding, pressure is applied with a sterile bandage for until bleeding has stopped. If the wound continues to bleed, medical attention at the nearest hospital is sought. The bat from which the bite or exposure originated is identified, and the samples collected from it labeled on the data sheet that these were involved in an exposure. Our procedures require that the person potentially exposed reports to a major hospital within 2 hours of exposure to receive a rabies booster (as per WHO/CDC recommendations). The samples collected will be placed in a viral transport buffer will be non-infectious. Samples placed in viral transport buffer will be stored at -86C until viral isolation is required. Serum will be heat inactivated (56C for 30 minutes) before testing.

Lab biosafety: Wuhan Institute of Virology and the WHO Collaborating Center for Animal Experimentation BSL-3 lab have an Internal Biosafety Committee and are accredited BSL-2 and BSL-3 laboratories. All experimental work using infectious material will be conducted under BSL-3 conditions.

Disposal of hazardous materials will be conducted according to BSL-3 procedures.

Bibliography & References

1. L. H. Taylor, S. M. Latham, M. E. J. Woolhouse, Risk factors for human disease emergence. *Philosophical Transactions of the Royal Society B: Biological Sciences* **362**, 2766-2775 (2007).
2. Y. Guan, B. J. Zheng, Y. C. Hu, Y. Li, J. Z. Yu, Z. H. Chen, C. W. Wang, B. H. Li, J. Zhang, Y. J. Guan, K. M. Butt, K. L. Wong, K. W. Chan, W. Lim, K. F. Shortridge, K. Y. Yuen, J. S. M. Peiris, J. L. M. Poon, Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. *Science* **302**, 276-279 (2003).
3. V. Li, Z. Shi, M. Yu, W. Ren, C. Smith, J. Y. Bestels, H. Wang, G. Crahan, J. Hu, H. Zhang, J. Zhang, J. McEachern, H. Field, P. Daszak, B. T. Eaton, S. Zhang, L. S. Wang, Bats are natural reservoirs of SARS-like coronaviruses. *Science* **310**, 676 (2005 Oct 28) (Epub 2005 Sep 2005).
4. W. D. Li, Z. L. Shi, M. Yu, W. Z. Ren, G. Yang, J. P. Xiao, J. McEachern, H. Field, P. Daszak, B. T. Eaton, S. Y. Zou, L. S. Wang, Bats are natural reservoirs of SARS-like coronaviruses. *Science* **310**, 676 (2005).
5. J. F. Drexler, V. M. Corman, T. Wegener, A. F. Jansen, R. M. Zerbinati, F. Gloza-Bausch, A. Seebens, M. A. Müller, C. Drosten, Amplification of a pathogenic virus in a bat colony. *Emerging Infectious Diseases* **17**, 449 (Mar, 2011).
6. J. Huynh, S. Li, B. Ye, A. Smith, L. Sturges, J. C. Olsen, J. Naqel, J. P. Simonsen, S. Agnihothram, J. E. Gao, M. B. Eisen, B. C. Davis, E. F. Donaldson, Evidence Supporting Zoonotic Origin of Human Coronavirus Strain NL63. *Journal of Virology* **86**, 12816 (Dec, 2012).
7. S. K. P. Lau, K. S. M. Li, Y. Huang, C. T. Shek, H. Tse, M. Wan, G. K. Y. Choi, L. Xu, C. S. F. Lam, R. T. Guo, K. H. Chan, B. J. Zheng, P. C. Y. Woo, Y. Yuan, Gen. Epidemiology and Complete Genome Comparison of Different Strains of Severe Acute Respiratory Syndrome-Related Coronavirus in Bats. *Journal of Virology* **84**, 2808 (Mar, 2010).
8. P. L. Quan, C. Firth, C. Street, J. A. Hargrett, A. Petrosny, A. Tashmukhamedova, S. K. Hutchison, M. Eglar, Identification of a Severe Acute Respiratory Syndrome Coronavirus-Like Virus in a Leaf-Nosed Bat, *Nigeria*. *Mbio* **1**, (Sep-Oct, 2010).
9. S. Tong, C. Conrardy, S. Ruone, I. V. Kuzmin, X. Guo, Y. Tao, M. Nie, S. Joda, L. Wang, R. F. Breiman, L. J. Anderson, C. E. Rupprecht, Detection of novel SARS-like and other coronaviruses in bats from Kenya. *Emerging Infect. Dis.* **15**, 482 (Mar, 2009).
10. M. Tahir, R. Gajraj, M. Bardhan, H. Mohammed, L. D. James, S. Chakrabarti, D. M. K. King, D. Killalea, K. James, M. Kemp, P. Duggal, K. Gan, M. Aiza, N. Agbogun, B. Sibai, K. Harari, O. Edeghere, K. Neal, S. Ibbotson, N. Wickramasinghe, N. Sherwood, B. Oppenheim, L. Hopton, H. Osman, E. Smit, S. Atabani, J. Workman, S. Wilson, C. Overton-Lewis, M. Logan, R. McCann, M. Petrovic, V. Bothra, W. Welfare, B. Isalska, J. Barker, A. Ashworth, I. Fedor, C. Seng, D. Kumar, B. McCloskey, R. Myers, R. Gopal, M. Zamban, P. K. Reddy, L. Thomas, N. Radhinatny, H. K. Green, Zh. Zaido, K. Kerheuy, I. Abubakar, J. Jones, N. Phin, M. Catchpole, C. M. Watson, H. T. S. K. H. Chan, Evidence of person-to-person transmission of a novel coronavirus in the United Kingdom. *Emerging Infectious Diseases* **19**, 1444 (2013).
11. A. Annan, H. J. Baldwin, V. M. Corman, C. M. Klöse, M. Owusu, E. E. Nkrumah, E. K. F. A. Agbenyega, B. Meyer, S. Oppong, A. Sarkodie, E. K. V. Kalko, P. H. C. Lina, E. V. Godlevskiy, Reusken, A. Seebens, F. Gloza-Bausch, P. Vainu, M. Tashmukhamedova, C. Drosten, J. F. Drexler, Human Betacoronavirus 2c EMC/2012-related Virus in Bats, Ghana and Further. *Emerging Infectious Diseases* **19**, 456 (2013-Mar, 2013).
12. S. Wacharapluengadee, C. Sintunawa, T. Kaewpom, K. Khongnornman, K. J. Olival, J. H. Epstein, A. Rodpan, P. Sangsri, N. Inta, H. A. Chindamporn, K. Suksawa, T. Hemachudha, Identification of Group 1C Betacoronavirus from Bat guano from Maezang, Thailand. *Emerging Infectious Diseases* **19**, 1444 (2013).
13. S. Anthony, J. M. Sánchez-Chávez, J. Navarrete-Macias, C. Zambra, J. H. Epstein, T. Tipps, E. Liang, M. Sangar, L. Leon, J. Sotomayor-Bou, A. C. A. de Medeiros, I. C. Goldstein, G. Sarzán-Bastak, V. A. Lipkin, Coronaviruses in bats from Mexico. *Journal of General Virology* **94**, (2013).

14. K. E. Jones, N. Patel, M. Ajay, S. Storey, D. H. Brown, J. L. Gittleman, P. Daszak, Global trends in emerging infectious diseases. *Nature* **451**, 990 (2008).
15. L. J. Saif, Animal coronaviruses: what can they teach us about the severe acute respiratory syndrome?
16. R. A. M. Fouchier, N. G. Hartwig, T. M. Bestebroer, B. Niemeyer, J. C. de Jong, A. C. Smit, A. Osterhaus, A previously undescribed coronavirus associated with respiratory illness in humans. *Proceedings of the National Academy of Sciences of the United States of America* **101**, 14960-14965 (2004).
17. E. C. Holmes, A new coronavirus and the emergence of a new class of virus. *Transactions of the Royal Society of London Series B, Biological Sciences* **359**, 1059 (2004).
18. L. Van der Hoek, K. Pyrc, M. F. Jebbink, V. Vermeulen-Oost, R. J. H. Berkhout, U. Viret, H. van den Brink, J. Kaandorp, J. Spaargaren, B. Berkhout, Identification of a new human coronavirus. *Nat Med* **10**, 368 (2004).
19. B. C. Fielding, Human coronavirus 229E: a clinically important coronavirus. *Emerging Infectious Diseases* **17**, 1000-1001 (2011).
20. S. Anthony, J. Epstein, K. Mulla, A. Flores, N. Islam, A. Islam, S. Ali Khan, P. Hosseini, I. Bogich, T. Goldstein, S. Luby, S. Morse, J. Mazet, P. Daszak, W. J. Linkin, Estimating viral diversity in bats. *Proceedings of the National Academy of Sciences*. (In Press).
21. R. H. Xie, L. H. Li, M. J. Moore, G. W. Davis, F. Li, L. H. Li, W. J. Liang, J. Y. Lin, A. Schnur, Epidemiologic clues to SARS origin in China. *Emerging Infectious Diseases* **10**, 1030 (Jun. 2004).
22. W. H. Li, M. J. Moore, N. Vasileva, J. H. Shi, S. K. Wong, M. A. Berne, M. Somasundaram, J. C. Sullivan, K. Luzuriaga, T. C. Greenough, H. Choe, M. Farzan, Angiotensin-converting enzyme 2 is a functional receptor for the novel coronavirus 229E. *Science* **305**, 1546-1548 (2004).
23. P.-L. Quan, C. Firth, C. Street, J. A. Henriquez, A. Petrosov, A. Tasmirki, A. Medvedeva, S. K. Hutchinson, M. Eghloun, M. O. V. Osipovi, M. Niezgod, A. B. Ounukova, T. Brase, G. Rupprecht, M. L. Linkin, Identification of a severe acute respiratory syndrome coronavirus-like virus in a leaf-nosed bat in Nigeria. *MBio* **1**, (2010).
24. D. Ribicari, P. Hostnik, A. Stever, J. Grom, I. Toplak, Identification of SARS-like coronaviruses in horseshoe bats. *Emerging Infectious Diseases* **16**, 1555-1567 (2010).
25. E. F. Donald, J. H. S. Kellum, E. Gates, S. Haynie, G. J. Moore, M. B. Hill, Analysis of the Genetic Diversity of North American Bat Species: Viral Diversity among Different Bat Species That Share a Common Habitat. *Journal of Virology* **84**, 13004 (Dec. 2010).
26. S. R. Dominguez, T. J. O'Shea, L. M. Oko, K. V. Holmes, Detection of Group 1 coronaviruses in North America. *Emerging Infectious Diseases* **13**, 1295 (Sep. 2007).
27. M. A. Müller, P. Paweska, P. A. Leifson, C. D. Steele, K. Conrath, M. Niedrig, S. Swanepoel, Coronavirus Antibodies in African Bat Species. *Emerging Infectious Diseases* **13**, 1367 (2007).
28. Y. Y. Ge, J.-L. Li, X.-L. Yang, A. Ashnam, M. E. Parham, P. Hu, W. Zhang, C. Peng, Y. Li, Zhang, C. M. Luo, B. Tan, N. Wang, Y. Zhu, G. Cramer, S. Li, L. Zhang, E. F. Wang, P. Daszak, Z. E. Shi, First isolation and characterization of bat SARS-like coronavirus that use the ACE2 receptor. *Nature*. (In Review).
29. D. S. Burke, in *Pathology of Emerging Infections*, A. M. Nelson, C. R. Horsburgh, Eds., Humana Press, 1998, pp. 1-12.
30. H. Tsunemitsu, Z. R. Elkanawati, D. R. Smith, H. H. Reed, L. J. Saif, Isolation of Coronaviruses Antigenically Indistinguishable from Bovine Coronavirus from a Human. *Clinical Microbiology* **33**, 3264 (Dec. 1995).
31. E. C. Holmes, A. J. Drummond, The evolutionary genetics of viral emergence. *Current Topics in Microbiology and Immunology* **58**, 1-12 (2007).
32. K. J. Olival, T. Bogich, C. Zambrana-Torrel, E. Loh, P. R. Hosseini, K. E. Jones, P. Daszak, Genetic phylogeny and the emergence of a novel coronavirus. *Emerging Infectious Diseases* **16**, 1000-1001 (2010).
33. D. G. Streicker, A. S. Turmelle, M. J. Vonhof, I. V. Kuznetsov, S. F. McCracken, C. E. Rupprecht, Host Phylogeny Constrains Cross-Species Emergence and Establishment of Rabies Virus in Diverse Mammals. *Science* **329**, 676 (Aug. 2010).
34. C. H. Calisher, J. E. Childs, H. E. Flanders, J. L. James, T. Schwaninger, Bats: Important reservoir hosts of emerging viruses. *Clinical Microbiology Reviews* **10**, 521 (Jul. 2000).

61. E. L. Haagmans, Dipeptidyl peptidase 4 is a functional receptor for the emerging human coronavirus-EMC. *Nature* **495**, 251 (Mar 14, 2013).
62. Y. X. Hou, C. Peng, M. Yu, Y. Li, Z. G. Han, F. L. Li, F. Wang, Z. L. Shi, Angiotensin-converting enzyme 2 (ACE2) proteins of different bat species confer variable susceptibility to SARS-CoV, *Archives of Virology* **155**, 1563 (Oct, 2010).
63. M. J. Bonnanarte, A. S. Dimitrov, K. N. Bossart, G. Cramer, B. A. Mungai, K. A. Bishop, V. Choudhry, D. S. Dimitrov, L. F. Wang, B. T. Eaton, C. C. Broder, Ephrin-B2 ligand is a functional receptor for Hendra virus and Nipah virus. *Proceedings of the National Academy of Sciences of the United States of America* **103**, 10662 (2006).
64. O. A. Negrete, M. J. Bonnanarte, C. C. Broder, B. T. Eaton, L. F. Wang, D. S. Dimitrov, EphrinB2 is the entry receptor for nipah virus, an emerging highly pathogenic paramyxovirus. *Nature* **435**, 270 (2005).
65. M. Yu, M. Tachibana, C. C. Broder, B. T. Eaton, L. F. Wang, D. S. Dimitrov, EphrinB2 is the entry receptor for nipah virus, an emerging highly pathogenic paramyxovirus. *Nature* **435**, 270 (2005).
66. J. O. Lloyd-Smith, D. George, E. H. Pepin, V. E. Fitzler, J. R. C. Pulliam, D. S. Cauley, D. Hudson, S. T. Grenfell, Epidemic dynamics at the interface of a reservoir and a new host: the case of respiratory syndrome coronavirus. *Journal of General Virology* **91**, 170 (Jul 2010).
67. S. Riley, G. M. Linton, C. A. Donnelly, A. C. Ghani, L. J. Simonsen, A. J. Valleron, A. J. Hedley, G. M. Leung, L.-M. Ho, T. H. Lam, T. Q. Trach, P. F. Tang, E. M. C. Lau, N. M. Ferguson, R. M. Anderson, Transmission dynamics of the etiological agent of severe acute respiratory syndrome. *Science* **300**, 1981 (2003).
68. R. M. Anderson, C. A. Donnelly, N. M. Ferguson, M. E. J. van Duynhoven, C. J. Watt, H. J. Udy, S. MaWhinney, S. P. Dunstan, P. F. Southwood, J. M. Williams, J. R. M. Ryan, J. L. Hoinville, L. F. Hillerton, A. R. Austin, G. A. H. Wells, Transmission dynamics of foot-and-mouth disease in cattle. *Nature* **382**, 779 (1996).
69. R. M. Anderson, R. M. May, Population biology of infectious diseases. Part 2. *Nature* **280**, 455 (1979).
70. R. M. Anderson, R. M. May, Population biology of infectious diseases. Part 1. *Nature* **280**, 402 (1979).
71. C. R. James, K. K. Corbett, J. H. Jones, J. Tröstle, Emerging infectious diseases: the role of social sciences. *Lancet* **384**, 1884 (Dec 2012).
72. B. T. Grenfell, O. G. Pybus, J. R. Gog, J. L. Wood, J. M. Daly, J. A. Miller, F. C. Minelli, M. J. B. Hill, The emergence, epidemiology and evolution of influenza A viruses. *Journal of Virology* **86**, 6305 (2012).
73. S. S. Morse, J. A. Miller, M. J. B. Hill, C. R. Parrish, D. Carroll, W. B. Karesh, C. Zambrana-Torreal, W. I. Lipkin, Influenza A virus evolution and emergence. *Journal of Virology* **86**, 6305 (2012).
74. T. L. Fuller, M. J. B. Hill, V. Martin, J. Cappelle, P. Hosseini, K. Y. Niabo, S. A. Azim, X. Xiao, P. Daszak, T. B. Smith, Predicting hotspots for influenza A virus emergence. *Emerging Infectious Diseases* **19**, 1000 (2013).
75. J. R. C. Pulliam, H. Epstein, J. Dushoff, S. A. Rahman, M. Bunning, A. A. Jamaluddin, A. D. Hyatt, H. E. Field, A. P. Dobson, P. Daszak, Emergent agricultural intensification, priming for persistence and the emergence of Nipah virus: a lethal bat-borne zoonosis. *Journal of Royal Society Interface* **9**, 20120101 (2012).
76. P. Hosseini, S. H. Sokolow, K. J. Vanderhoff, A. M. Kilpatrick, P. Daszak, D. B. Clark, and socio-economic data for early pandemic spread. *PLOS ONE* **5**, e12767 (2010).
77. A. M. Kilpatrick, C. A. Chmura, D. W. Gibbons, R. C. Fleischer, P. P. Marra, P. Daszak, Predicting global spread of H5N1 avian influenza. *Proceedings of the National Academy of Sciences of the United States of America* **103**, 1957 (2006).
78. W. Ren, X. G. Wu, D. Li, Z. G. Han, M. Yu, P. Zhou, S. Y. Zhang, L. F. Wang, H. K. Deng, Z. L. Shi, Difference in receptor usage between severe acute respiratory syndrome (SARS) coronavirus and SARS-like coronavirus of bat origin. *Journal of Virology* **84**, 1100 (2010).
79. V. S. Raj, H. Mou, S. L. Smits, D. H. Dekkers, M. A. Muller, R. Dijkman, D. Mut, P. F. M. S. Zaki, K. A. I. Uebachs, V. Thielen, D. S. Dimitrov, Dipeptidyl peptidase 4 is a functional receptor for the emerging human coronavirus EMC. *Nature* **495**, 251 (Mar 14, 2013).
80. D. V. Sridhar, G. L. D. Smith, J. X. Zhang, Y. S. M. Peiris, H. Chen, Y. Guan, Evolutionary insights into the ecology of coronaviruses. *Journal of Virology* **81**, 4012 (Apr. 2007).

71. R. Antia, R. R. Rego, Y. C. Koella, E. Bergelson, The role of host immunity in infectious diseases. *Nature* **400**, 658 (2002).
72. A. Dobson, Population dynamics of pathogens with multiple host species. *Am Nat* **164**, 564 (Jan 1, 2004).
73. O. Diekmann, J. A. P. Heesterbeek, J. A. J. Metz, On the Definition and the Computation of the Basic Reproduction Ratio R_0 in Models for Infectious Diseases in Heterogeneous Populations. *Journal of Mathematical Biology* **28**, 365 (1990).
74. V. Nijman, An overview of international wildlife trade from Southeast Asia. *Biodiversity and Conservation* **19**, 1101 (Apr 2010).
75. L. Yiming, L. Dianmo, A Preliminary Investigation on the Status of the Wildlife Trade in Guangxi, China. *Chinese Biodiversity* **4**, 57 (1999).
76. L. Yiming, L. Dianmo, The dynamics of trade in live wildlife across the Guangxi border between China and Vietnam during 1993-1996 and its control strategy. *Conservation Biology* **11**, 103 (1997).
77. A. Patz, E. Vugler, J. Guerrero, N. Hayes, B. Murphy, B. Sarki, K. Subbarao, Severe Acute Respiratory Syndrome Coronavirus Infection in Golden Syrian Hamsters. *J. Virol.* **79**, 503 (Jan 15, 2005).
78. L. K. D. Luna, V. Heiser, N. Tegamey, M. Panning, J. F. Drexler, S. Muirang, L. Hanson, S. Baumgarte, B. J. Haijema, L. Kaiser, C. Drosten, Generic detection of coronaviruses and differentiation at the prototype strain level by reverse transcription-PCR. *Journal of Clinical Microbiology* **45**, 1049 (2007).
79. D. Bell, S. Robertson, P. R. Hunter, Animal origins of SARS coronavirus: possible links with the international trade in small carnivores. *Philosophical Transactions of the Royal Society of London Series B, Biological Sciences* **359**, 1811 (2004).
80. X. Xu, Y. Q. Liu, S. Weiss, E. Amaki, S. G. Sarafianos, S. T. Ding, Molecular model of SARS coronavirus polymerase: functions and implications. *Structure* **11**, 7117 (Dec 15, 2003).
81. X. C. Tang, G. Li, N. Vasilakis, Y. Zhang, L. L. Shi, Y. Zhong, L. F. Wang, S. Y. Zhang, Differential expression of SARS-CoV-2 in various tissues. *Journal of Virology* **83**, 10000 (Mar 2009).
82. S. K. P. Lau, P. C. Y. Woo, K. S. M. Li, Y. Huang, H. W. Leung, K. H. Chan, Y. Y. Li, N. Severe acute respiratory syndrome coronavirus in Chinese horseshoe bats. *Proceedings of the National Academy of Sciences of the United States of America* **102**, 14040 (Sep, 2005).
83. J. Yuan, C. C. Hong, D. Wang, C. Y. Hu, D. Zhu, L. P. Tu, T. Tu, F. Q. Guo, Z. Shi, Intraspecies diversity of SARS-like coronaviruses in *Rhinolophus sinicus* and its implications for the origin of SARS coronavirus in humans. *Journal of Virology* **80**, 10000 (2006).
84. S. Watanabe, J. S. Masangkay, N. Nagata, S. Iwionkawa, T. Mizutani, S. Fukushima, P. A. Alvioia, I. Omatsu, N. Ueda, K. Iha, S. Taniguchi, M. Fujii, S. Tsuda, M. Endoh, K. Kato, Y. Tohya, S. Kiyawa, Y. Yoshikawa, H. A. B. The origin of Bats, the Philippines. *Emerging Infectious Diseases* **16**, 1017 (Apr, 2010).
85. J. Sheahan, B. Rockx, E. Donaldson, D. C. S. B. Paris, Pathways to synthetic reconstruction of a synthetic severe acute respiratory syndrome coronavirus. *Journal of Virology* **82**, 8721 (2008).
86. H. D. Song, C. C. Tu, G. W. Zhang, S. Y. Wang, K. Zheng, L. C. Lu, Q. R. Zhou, H. Zhou, Y. F. Liu, L. F. He, B. Z. Qin, L. H. Li, Y. Q. Ren, W. J. Liang, Y. D. Xu, L. Anderson, M. Wang, R. H. Xu, X. W. Wu, H. Y. Zheng, J. D. Chen, G. D. Liang, Y. Gao, M. J. Fang, J. Y. Jiang, H. F. Chen, B. Di, L. J. He, J. Y. Lin, S. J. Wang, X. G. Kong, L. Du, P. Hao, H. Tang, W. O. Spiga, Z. M. Guo, H. Y. Pan, W. Z. He, J. C. Manuayan, A. Fontana, A. Danchin, N. N. Gai, Y. X. Li, C. I. Wu, J. S. B. Cross-host evolution of severe acute respiratory syndrome coronavirus from civet to human. *Proceedings of the National Academy of Sciences of the United States of America* **102**, 2430 (Feb, 2005).
87. S. Koh, K. Kuma, H. Saito, Multiple sequence alignment. *Nucleic Acids Res.* **24**, 1000 (1996).
88. A. Stamatakis, Rapidly accurate distance-based phylogenetic analyses with taxa and mixed models. *Bioinformatics* **22**, 2688 (2006).

CONSORTIUM/CONTRACTUAL ARRANGEMENTS

Consortium/Contractual Arrangements

This project is a multi-institutional collaboration led by EcoHealth Alliance, New York (Daszak, PI), which will subcontract funds to two institutions: the East China Normal University (Dr. S. Zhang) and the Wuhan Institute of Virology (Dr. Shi), both foreign institutions. Dr. Daszak has over 15 years of managing contracts with these institutions, a 5-year NIAID Ecology of Infectious Diseases award on West Nile virus with subcontractees, an R01 on bat viral diversity that involves multiple international contracts, a 1.5 million dollar p.a. contract from the National Institute of Health (NIH) (EcoHealth Alliance) is justified in taking the lead on this project, and virology and epidemiology. Preliminary work on this issue, including 10 years of research on the ecology and evolution of the emergence of SARS and 11-years of work in China. The subcontractees will work on specific issues and areas in which they have proven expertise. These areas are: human and animal sampling (East China Normal University, Dr. Zhang) and viral discovery, pathogenesis as well as sample storage and shipping (Wuhan Institute of Virology, Dr. Shi). Dr. Daszak has collaborated with Dr. Zhang for 8 years, and Dr. Shi for 10 years, and has been involved in contractual arrangements with ECNU for 8 years. Dr. Shi and Dr. Zhang have collaborated together since 2002 and have been involved in running joint conferences, and shipping samples into and out of China.

RESOURCE SHARING PLAN

Data Sharing Plan: Sequence data will be made publicly available via GenBank, and by other scientists, as soon as a publication is in press. Viral isolates will be made available to Virology initially. Isolates, reagents and any other products, should they be developed, will be made available to other scientists through Transfer Agreements and/or licensing agreements.

Sharing Model Organisms: We do not anticipate the development of model organisms. Should any be developed, they will be made available to the scientific community through the National Center for Genome Resources (NCGR) Genome Wide Association Consortium (GWAS) NIA.

1. Application Type:

From SF 424 (PHS) R1 Cover Page. The resubmission, renewal, continuation, and revision R&R cover page are repeated here for your reference, as you answer the questions that are specific to the PHS308.

* Type of Application:

- New
- Resubmission
- Renewal
- Continuation
- Revision

Federal Identifier: GRANT11418218

2. Change of Principal Investigator / Change of Institution Questions

Change of Principal Investigator

Name of former principal investigator / program director:

Prefix:

First Name:

Middle Name:

* Last Name:

Suffix:

Change of Grantee Institution

* Name of former institution:

3. Inventions and Patents (For renewal applications only)

* Inventions: Yes No

Answer:

* Previously Reported: Yes No

4. * Program Income

Is program income expected to be generated by this project during the project period?

Yes No

If you checked "yes", please provide the following information:

Year	Amount	Source
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<input type="text"/>	<input type="text"/>	<input type="text"/>
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5. * Disclosure of Potential Conflicts of Interest Statement

If this applicant or investigator has a financial interest in any organization that may be interested in contacting you for further information (e.g., a company, a consultant, or a partner), please disclose the nature of the interest.

Yes No